

MARKED-UP COPY OF SPECIFICATION

Page 7, line 23,-Page 8, lines 1-15:

The present invention also particularly concerns peptide variants whose sequence does not completely correspond to the above-mentioned amino acid sequences but which have the same or closely related "anchor positions". In this connection the terms "anchor position" means an amino acid residue essential for binding to a MHC molecule in particular to a MHC molecule of classes DR3, DR4 or DQ. The anchor positions for the DRB10401 binding motive are for example given in Hammer et al., Cell 74 (1993), 197-203. Hammer states that "[t]he amino acid composition of all identified anchors and the deduced MHC class II allele-specific binding motifs are summarized in Table III. Comparing the motifs identified for the three alleles, we see that while the anchors at positions 1 and 4 are practically invariant, the anchors at position 6 differ among the three DR alleles. This suggests that residues at this position confer allelic specificity to the binding. Table III is attached below.

TABLE III

Relative Position									
	1	2	3	4	5	6	7	8	9
ORB1*0101	Y* (47%) F (26%)	X	X	M (48%) L (28%)	X	A (34%) G (23%) S (09%)	X	X	L (43%) M (13%) A (13%)
DRB1*0401	W (43%) Y (31%)	X	X	M (23%) A (19%) V (13%) L (12%)	X	T (60%) S (12%)	L (34%) Q (20%) M (10%) N (10%)	X	X
DRB1*1101	W (67%)	X	X	M (33%) L (23%) V (13%)	X	R (61%) K (12%)	X	X	X

Such anchor positions are conserved in peptides according to the invention or optionally replaced by amino acid residues with chemically very closely related side-chains (e.g. alanine by valine, leucine by isoleucine and vice versa). The anchor positions in the peptides according to the invention can be determined in a simple manner by testing variants of the above-mentioned specific peptides for their binding capability to MHC molecules. Peptides according to the invention are characterized in that they exhibit an essentially equivalent specificity or/and affinity of binding to MHC molecules as the aforementioned peptides. The peptides derived from peptides having the amino acid sequences (I) or (II) or from the amino acid sequences shown in Figures 1 and 2

preferably have a sequence homology of at least 40%, particularly preferably of at least 50% and most preferably of at least 60% to the parent peptides or partial sequences thereof.